

M. Dibrino



RAW SEQUENCE LISTING DATE: 02/28/2002  
PATENT APPLICATION: US/09/652,282 TIME: 15:01:42

Input Set : N:\Crif3\RULE60\09652282.txt  
Output Set: N:\CRF3\02282002\I652282.raw

SEQUENCE LISTING

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MAR 06 2002  
TECH CENTER 1600/2900

ENTERED

- 4 (1) GENERAL INFORMATION:
- 6 (i) APPLICANT: Gately, Maurice K.
- 7 Presky, David H.
- 9 (ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12
- 11 (iii) NUMBER OF SEQUENCES: 4
- 13 (iv) CORRESPONDENCE ADDRESS:
- 14 (A) ADDRESSEE: Hoffmann-La Roche Inc.
- 15 (B) STREET: 340 Kingsland Street
- 16 (C) CITY: Nutley
- 17 (D) STATE: New Jersey
- 18 (E) COUNTRY: United States
- 19 (F) ZIP: 07110-1199
- 21 (v) COMPUTER READABLE FORM:
- 22 (A) MEDIUM TYPE: Floppy disk
- 23 (B) COMPUTER: IBM PC compatible
- 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 27 (vi) CURRENT APPLICATION DATA:
- C--> 28 (A) APPLICATION NUMBER: US/09/652,282
- C--> 29 (B) FILING DATE: 30-Aug-2000
- 30 (C) CLASSIFICATION:
- 33 (vii) PRIOR APPLICATION DATA:
- 34 (A) APPLICATION NUMBER: 09/232,522
- 35 (B) FILING DATE:
- 38 (viii) ATTORNEY/AGENT INFORMATION:
- 39 (A) NAME: Buchholz, Briana C.
- 40 (B) REGISTRATION NUMBER: 39,123
- 41 (C) REFERENCE/DOCKET NUMBER: CD 1048P
- 43 (ix) TELECOMMUNICATION INFORMATION:
- 44 (A) TELEPHONE: 973-235-6208
- 45 (B) TELEFAX: 973-235-2363
- 48 (2) INFORMATION FOR SEQ ID NO: 1:
- 50 (i) SEQUENCE CHARACTERISTICS:
- 51 (A) LENGTH: 321 base pairs
- 52 (B) TYPE: nucleic acid
- 53 (C) STRANDEDNESS: double
- 54 (D) TOPOLOGY: linear
- 56 (ii) MOLECULE TYPE: cDNA
- 58 (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO
- 62 (vi) ORIGINAL SOURCE:
- 63 (A) ORGANISM: mouse

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64      (G) CELL TYPE: Hybridoma
65      (H) CELL LINE: HIL-12F3-16G2
66      (ix) FEATURE:
67          (A) NAME/KEY: CDS
68          (B) LOCATION: 1..321
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC      48
76 Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
77   1           5           10           15
79 CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC      96
80 Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
81           20           25           30
83 TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA      144
84 Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
85           35           40           45
87 AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC      192
88 Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
89   50           55           60
91 TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT      240
92 Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
93 65           70           75           80
95 TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT TAC TGT GCA AGA TCT TCG      288
96 Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
97           85           90           95
99 GAT GCT TTG GAC TAC TGG GGC GCA GGG ACC ACG      321
100 Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
101   100           105
104 (2) INFORMATION FOR SEQ ID NO: 2:
106     (i) SEQUENCE CHARACTERISTICS:
107         (A) LENGTH: 107 amino acids
108         (B) TYPE: amino acid
109         (D) TOPOLOGY: linear
111     (ii) MOLECULE TYPE: protein
113     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
115 Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
116   1           5           10           15
118 Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
119           20           25           30
121 Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
122           35           40           45
124 Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
125           50           55           60
127 Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
128 65           70           75           80
130 Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
131           85           90           95
133 Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
134   100           105
136 (2) INFORMATION FOR SEQ ID NO: 3:

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138      (i) SEQUENCE CHARACTERISTICS:
139          (A) LENGTH: 308 base pairs
140          (B) TYPE: nucleic acid
141          (C) STRANDEDNESS: double
142          (D) TOPOLOGY: linear
144      (ii) MOLECULE TYPE: cDNA
146      (iii) HYPOTHETICAL: NO
148      (iv) ANTI-SENSE: NO
150      (vi) ORIGINAL SOURCE:
151          (A) ORGANISM: mouse
152          (G) CELL TYPE: Hybridoma
153          (H) CELL LINE: HIL-12F3-20E11
155      (ix) FEATURE:
156          (A) NAME/KEY: CDS
157          (B) LOCATION: 1..306
160      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
162 GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC      48
163 Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu
164   1      5      10      15
166 ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG      96
167 Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp
168      20      25      30
170 ATC CGG AAA TTC CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA AGT      144
171 Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser
172      35      40      45
174 TAC AGT GGT AGT ACT TAC TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC      192
175 Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser
176      50      55      60
178 ATC ACT CGA GAC ACA TCC AAG AAC CAG TAC TCC ATG CAG TTG AAT TCT      240
179 Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser
180      65      70      75      80
182 GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TCC TCG GAT      288
183 Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp
184      85      90      95
186 GCT ATG GAC TAC TGG GGC GC      308
187 Ala Met Asp Tyr Trp Gly
188      100
191 (2) INFORMATION FOR SEQ ID NO: 4:
193      (i) SEQUENCE CHARACTERISTICS:
194          (A) LENGTH: 102 amino acids
195          (B) TYPE: amino acid
196          (D) TOPOLOGY: linear
198      (ii) MOLECULE TYPE: protein
200      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
202 Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu
203   1      5      10      15
205 Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp
206      20      25      30
208 Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser

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209		35		40		45													
211	Tyr	Ser	Gly	Ser	Thr	Tyr	Tyr	Asn	Pro	Ser	Leu	Arg	Ser	Arg	Ile	Ser			
212		50					55					60							
214	Ile	Thr	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Tyr	Ser	Met	Gln	Leu	Asn	Ser			
215	65					70					75					80			
217	Val	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	Ala	Arg	Ser	Ser	Asp			
218					85					90					95				
220	Ala	Met	Asp	Tyr	Trp	Gly													
221					100														

VERIFICATION SUMMARY                      DATE: 02/28/2002  
PATENT APPLICATION: US/09/652,282        TIME: 15:01:43

Input Set : N:\Crf3\RULE60\09652282.txt  
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]